

Query Match	88.5%	Score 2950	DB 4	Length 3544
Best Local Similarity	95.0%	Pred. No. 0		
Matches 3135	Conservative	0	Mismatches	0
			Indels	165
			Gaps	2
QY	197	GCTTTCACTCAAGTAAAGCTGTTGGAGCGCGGAGCCAAAGTTAAAGATTGATGTATG	256	
Db	224	GCTTTCACTCAAGTAAAGCTGTTGGAGCGCGGAGCCAAAGTTAAAGATTGATGTATG	283	
QY	257	CGTGCCTCTCCAAAGCATCTTTGTGTGGAAAGTATTTCAGTCATCTCTTATATG	316	
Db	284	CGTGCCTCTCCAAAGCATCTTTGTGTGGAAAGTATTTCAGTCATCTCTTATATG	343	
QY	317	ATCAATGTGAGGGCTCTTTGTGACCGAAGTCTTTTGCAAGACATTCACCGGAAA	376	
Db	344	ATCAATGTGAGGGCTCTTTGTGACCGAAGTCTTTTGCAAGACATTCACCGGAAA	403	
QY	377	GAGAAAGACATTCATCTGGAGGGCTCTTGCCTGAAAAATGGATTAACTCTCTTTGGC	436	
Db	404	GAGAAAGACATTCATCTGGAGGGCTCTTGCCTGAAAAATGGATTAACTCTCTTTGGC	463	
QY	437	AGTCACACACCTGACCTCATACATCACTTTTGTGCAATGAGAGGCGTAGACCTTTGAC	496	
Db	464	AGTCACACACCTGACCTCATACATCTTTTGTGCAATGAGAGGCGTAGACCTTTGAC	523	
QY	497	ACGCCACTTTCATATCTGTGGCAATTAAAGAGAGCTGGAAAAAGAGACTTATTG	556	

Db 524 AACACCAATTACATATGTCGCAAAATTAAAGAGAGTGGAAAAAGCACTTATTG 583
QY 557 TTGTCAATGCCCCATGAGATGATGGAACTCAAAATTGTACTAGAGAGTGGTGGCTCTGC 616
Db 584 TTGTCAATGCCCCATGAGATGATGGAACTCAAAATTGTACTAGAGAGTGGTGGCTCTGC 643
QY 617 TGGAAAGTGGAAAGGAAAAAGTGTGCTAAATGATAGCCGCACTTTGTGAAATACATA 676
Db 644 TGGAAAGTGGAAAGGAAAAAGTGTGCTAAATGATAGCCGCACTTTGTGAAATACATA 703
QY 677 CATCCCACTTTTGGAAAGCAATTAATATCAATGCTCCAGGCTTAAGAAAGGAGTGGC 736
Db 704 CATCCCACTTTTGGAAAGCAATTAATATCAATGCTCCAGGCTTAAGAAAGGAGTGGC 763
QY 737 AACAGCAAAAGTTTAATTAAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACA 796
Db 764 AACAGCAAAAGTTTAATTAAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACA 823
QY 797 TTGATTCAGTCAAGAGGTTGATTAAGATCAAGCTCCAGAGTGTGCTCTCTCT 856
Db 824 TTGATTCAGTCAAGAGGTTGATTAAGATCAAGCTCCAGAGTGTGCTCTCTCTCT 883
QY 857 CTTCAAGCTTTTCTCACTGTACTCTGCGGTAACTGAGAAAGGCTTCAACCTGTTC 916
Db 884 CTTCAAGCTTTTCTCACTGTACTCTGCGGTAACTGAGAAAGGCTTCAACCTGTTC 943
QY 917 ACCGTCTGC----- 926
Db 944 ACTGCTTGAAGGTGGTTTGTGATGTTCTCTGTTGTTTCCGTGGCCTGTGAAAGAA 1003
QY 927 ----- 926
Db 1004 AATCACTCTATGCTCTACTGCACTTCTCAGCCTTGTACTACTGTCGCAATTTGGC 1063
QY 927 -----AGAGC 932
Db 1064 CAACCCGAATTCCTCCCAATCTTATCTTGGCTGGCAGAGATGTCTCAAGAGAGC 1123
QY 933 TGATGACAGAGAAATGGGATTGGTTAAGTGTAAATGCCAGCAATCTGTCCAAAGCTTC 992
Db 1124 TGATGACAGAGAAATGGGATTGGTTAAGTGTAAATGCCAGCAATCTGTCCAAAGCTTC 1189
QY 993 ACTTTATCCCCAGTCTCAATTTCTGCGTGTGCTGTATGACAGCTTTTGTGAGAAA 1052
Db 1184 ACTTTATCCCCAGTCTCAATTTCTGCGTGTGCTGTATGACAGCTTTTGTGAGAAA 1243
QY 1053 TTTTGCCTGTGTGACAAATCAGTATGATTCATTGAGAAAGCAAAAGCTTCCATGAT 1112
Db 1244 TTTTGCCTGTGTGACAAATCAGTATGATTCATTGAGAAAGCAAAAGCTTCCATGAT 1303
QY 1113 GTGTTCTAGTGCACCTGTTTATGCTGGATCTCCCGCTCCGCAACATGGCTATGCTTACA 1172
Db 1304 GTGTTCTAGTGCACCTGTTTATGCTGGATCTCCCGCTCCGCAACATGGCTATGCTTACA 1363
QY 1173 TCATGAAAGAGATGACATGCTTTTAAATGAGCTTACAGATTTGTGAAAGAAAAAGAC 1232
Db 1364 TCATGAAAGAGATGACATGCTTTTAAATGAGCTTACAGATTTGTGAAAGAAAAAGAC 1423
QY 1233 CTACTATATCTCAAACTTCAATTTTCTGCGCACTCTGAGACTATGAGAAAGATTA 1292
Db 1424 CTACTATATCTCAAACTTCAATTTTCTGCGCACTCTGAGACTATGAGAAAGATTA 1483
QY 1293 AGAACAAGACTGAGAGATCAAGGCAAGAGCAAACTCAAGCTGTCTCACTGAGAGAC 1352
Db 1484 AGAACAAGACTGAGAGATCAAGGCAAGAGCAAACTCAAGCTGTCTCACTGAGAGAC 1543
QY 1353 CAATGAAAGCTGTCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGGAGACCCCTCTAGTC 1412
Db 1544 CAATGAAAGCTGTCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGGAGACCCCTCTAGTC 1603
QY 1413 CAACCTGTGCGAGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGGAGACCCCTCTAGTC 1472
Db 1604 CAACCTGTGCGAGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGGAGACCCCTCTAGTC 1663

QY 1473 GCGTGCAGAGCGTGGCCAGCGTGCAGCGGTGCTGTTTAAAGAGACGCCGCTGTACAG 1532
Db 1664 GCGTGCAGAGCGTGGCCAGCGTGCAGCGGTGCTGTTTAAAGAGACGCCGCTGTACAG 1723
QY 1593 CGCTCAGTGGCTGACCTGTGCGCAGACAGAGCTGAAAGACAGCAATTAAGCTAAGCTT 1592
Db 1724 CGCTCAGTGGCTGACCTGTGCGCAGACAGAGCTGAAAGACAGCAATTAAGCTAAGCTT 1783
QY 1593 CTTTCTCTCTGATATCAAAATGATTTTCAATTTTCAAGCCAGCATGGCAGATCTCTTACG 1652
Db 1784 CTTTCTCTCTGATATCAAAATGATTTTCAATTTTCAAGCCAGCATGGCAGATCTCTTACG 1843
QY 1653 GCTTCTCTCTATCAGAAAGATGCTTTGGAAATCTACAAACTTTCAGTACTGTGATGGGA 1712
Db 1844 GCTTCTCTCTATCAGAAAGATGCTTTGGAAATCTACAAACTTTCAGTACTGTGATGGGA 1903
QY 1713 CCACAAAGCTATGCAAGTTCCTCCCTGTTCAAGAACTATCCGAGACAGACTCCGAAACCA 1772
Db 1904 CCACAAAGCTATGCAAGTTCCTCCCTGTTCAAGAACTATCCGAGACAGACTCCGAAACCA 1963
QY 1773 GTCTGTATTAAGAGAGAGAGCCAGATCCCAAGAGCTGACAGCCGAGGCTTACAGAA 1832
Db 1964 GTCTGTATTAAGAGAGAGAGCCAGATCCCAAGAGCTGACAGCCGAGGCTTACAGAA 2023
QY 1893 GCGAAGCAAGCGATTCATTCGATCAAGACAGAGAGTGGCACTGCCAGAGGTGCC 1892
Db 2024 GCGAAGCAAGCGATTCATTCGATCAAGACAGAGAGTGGCACTGCCAGAGGTGCC 2083
QY 1893 TTTTATCTCTCACTGATGAGAGTGGAGGTGAGAGCAATTAACACAGCTTCTCTT 1952
Db 2084 TTTTATCTCTCACTGATGAGAGTGGAGGTGAGAGCAATTAACACAGCTTCTCTT 2143
QY 1953 TGGGCTTTCCACAGCAGCAGAGAGACCTCAAGAACTGTCGCGCTGAGGCTTAAGGCT 2012
Db 2144 TGGGCTTTCCACAGCAGCAGAGAGACCTCAAGAACTGTCGCGCTGAGGCTTAAGGCT 2203
QY 2013 GGCATCTCGAATCTTGGGCCCCCAACCTCTTACCCTTCCCTGACAGCACTGCTATT 2072
Db 2204 GGCATCTCGAATCTTGGGCCCCCAACCTCTTACCCTTCCCTGACAGCACTGCTATT 2263
QY 2073 TTGCAAGAGTCTCAACATTTACTGTGCTCAAGCATTAAGAGAGAGAGTGGCACT 2132
Db 2264 TTGCAAGAGTCTCAACATTTACTGTGCTCAAGCATTAAGAGAGAGAGTGGCACT 2323
QY 2133 ACTGTGCTTACAGCTGACAGCAGCTGCCCACTTGGAGAGACAACTCTATTCTGTGCGCA 2192
Db 2324 ACTGTGCTTACAGCTGACAGCAGCTGCCCACTTGGAGAGAGCAAGCTCTATTCTGTGCGCA 2383
QY 2193 GGGGCAAGAGCAAGTGAAGAGCTGATCTCGCGGCGAGAGCTGGCATGAAGAGAGCTCT 2252
Db 2384 GGGGCAAGAGCAAGTGAAGAGCTGATCTCGCGGCGAGAGCTGGCATGAAGAGAGCTCT 2443
QY 2253 TTGAAAGAGCTTTAAAGCAAGAGTGGCAATATGAAATTTGAGAGAGCATCATGTCG 2312
Db 2444 TTGAAAGAGCTTTAAAGCAAGAGTGGCAATATGAAATTTGAGAGAGCATCATGTCG 2503
QY 2313 AGAACAAGTCAAGGAGAGAGCTGGGAAAGTGGCAGTCACTAGCTTTTCCGAGAGCA 2372
Db 2504 AGAACAAGTCAAGGAGAGAGCTGGGAAAGTGGCAGTCACTAGCTTTTCCGAGAGCA 2563
QY 2373 TGGAAATCAATTAAGGTCTCTGAGAAAGAAAGACATTTGTGACTTCTTAAACAATTTT 2432
Db 2564 TGGAAATCAATTAAGGTCTCTGAGAAAGAAAGACATTTGTGACTTCTTAAACAATTTT 2623
QY 2433 TTTCTTGTTCACAAAATTTCTCTGTAATTTGAAATATATATATATATATATATAT 2492
Db 2624 TTTCTTGTTCACAAAATTTCTCTGTAATTTGAAATATATATATATATATATATAT 2683
QY 2493 ATTTTGGAAAAATGAGCTATGCTTAAAGAGCAAGGTGATCAACCCAGTTTATCTC 2552
Db 2684 ATTTTGGAAAAATGAGCTATGCTTAAAGAGCAAGGTGATCAACCCAGTTTATCTC 2743

2553 TCTTACATCTGCAATTGAGAGATCAGTAATACTCTCTCAACAAAATGAGAGGAG 2612
2744 TCTTACATCTGCAATTGAGAGATCAGTAATACTCTCTCAACAAAATGAGAGGAG 2803
2613 ATGCTAGAAATCCCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2672
2804 ATGCTAGAAATCCCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2863
2673 TGTCTTAAATGAG 2732
2864 TGTCTTAAATGAG 2922
2733 GTTGTGCTACTAG 2792
2923 GTTGTGCTACTAG 2982
2793 TAGCGCTAG 2852
2983 TAGCGCTAG 3042
2853 TAGCTGTAATGAG 2912
3043 TAGCTGTAATGAG 3102
2913 TGAAG 2972
3103 TGAAG 3162
2972 TCTTACCTTAAAG 3032
3163 TCTTACCTTAAAG 3222
3033 ATCTGCTAG 3092
3223 ATCTGCTAG 3182
3093 CCAATTCAG 3152
3283 CCAATTCAG 3242
3153 CTTCTCAGCTTAAAG 3212
3243 CTTCTCAGCTTAAAG 3302
3213 TGGCAAGTACAG 3272
3403 TGGCAAGTACAG 3362
3273 AATCAAGATGTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3332
3463 AATCAAGATGTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3422

RESULT 2
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 3852 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Query Match 49.8%; Score 1660; DB 4; Length 1998;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 0; Indels 164; Gaps 1;
562 ATGGCCCTTAAAG 621
1 ATGGCCCTTAAAG 60
622 ATGGAG 681
61 ATGGAG 120
682 CACATTTGAG 741
121 CACATTTGAG 180
742 GACAAAGTAAATTAAG 801
181 GACAAAGTAAATTAAG 240
802 TGCAGTAAAG 861
241 TGCAGTAAAG 300
862 GACTGTTTCTCAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 921
301 GACTGTTTCTCAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
922 CTGTC----- 926
361 CTGTCAG 420
927 ----- 926
421 ACTGATGCTTACCTGATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
927 ----- 926
481 GAAATTCCTCCAACTTAACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
938 CAG 997
541 CAG 600
998 ATCCCGAGTCTCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
601 ATCCCGAGTCTCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
1058 CCGTGTGAG 1117
661 CCGTGTGAG 726
1118 CTAGTGAAGTCTGAG 1177
721 CTAGTGAAGTCTGAG 780
1178 AAG 1237
781 AAG 840
1238 ATATCTCAAACTTCAATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1297
841 ATATCTCAAACTTCAATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
1298 CAG 1357
901 CAG 960
1358 GAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1417
961 GAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2004, 00:57:54 ; Search time 110 Seconds

2608.269 Million cell updates/sec

Title: US-09-964-277-21

Sequence: 1 M¹PLSLQTVFSLYFMVNR...LGKVGSGSFGSMBIIEVS 517

Scoring table: OLIGO

Searched: 682709 seqs, 277475446 residues

Word size:

Total number of hits satisfying chosen parameters: 1360453

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-Q=csnr2.1/USPFO/US039964277/rnaata32022040.085402.2228/app_query.fasta.1.71
-DeIsolated_Patents_NA.-OPM=fastad.-SURF=clpdm.rm1.-RNA=chr0.1.-LOCP=0
-LOOPEXT=0.-UNITS=516.-START=1.-END=1.-MAPTX=clpdm.-TRANS=unmado.cdi
-LIST=45.-DOCALLIGN=200.-TRP SCORE=quality.-TRM MIN=1.-ALIGN=15.-MODE=LOCAL
-OUTPM=pmc.-NORM=ext.-HEADSIZE=500.-MAXLEN=2000000000
-USR=US039964277.GCC4.1.1.36.6.refmat.23022040.085402.2228.-NGCP=6
-NO_MMAP.-LARGESORT.-NGC SCORES=0.-MAT.-DSBLOC=100.-XGAPEXT=60
-DEVELOPER=7.-YGAPOF=60.-YGAPEXT=60.-XGAPEXT=60.-FGAPDF=6
-DEVELOPER=7.-YGAPOF=60.-YGAPEXT=60.-XGAPEXT=60.-FGAPDF=6
-DEVELOPER=7.-YGAPOF=60.-YGAPEXT=60.-XGAPEXT=60.-FGAPDF=6
```

Database :

```

1: /cgm2_6/prodata/2/ina/5B COMB.seg.*
2: /cgm2_6/prodata/2/ina/5A COMB.seg.*
3: /cgm2_6/prodata/2/ina/6A COMB.seg.*
4: /cgm2_6/prodata/2/ina/6B COMB.seg.*
5: /cgm2_6/prodata/2/ina/PCPTS COMB.seg.*
6: /cgm2_6/prodata/2/ina/backfiles1.seg.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	488	94.4	1995	4	US-09-816-494-3	Sequence 3, Appl1
2	488	94.4	2344	4	US-09-816-469-1	Sequence 1, Appl1
3	20	3.9	2377	4	US-09-820-668-3	Sequence 3, Appl1
4	12	2.3	2109	4	US-09-016-433-1135	Sequence 1135, Appl1
5	12	2.3	2109	4	US-09-023-655-9946	Sequence 946, Appl1
6	9	1.7	320	4	US-09-389-681-310	Sequence 310, Appl1
7	9	1.7	320	4	US-09-820-405B-110	Sequence 310, Appl1
8	9	1.7	320	4	US-09-339-338-310	Sequence 310, Appl1
9	9	1.7	320	4	US-09-433-423B-110	Sequence 310, Appl1
10	9	1.7	320	4	US-09-433-283A-110	Sequence 310, Appl1
11	9	1.7	320	4	US-09-834-781-310	Sequence 310, Appl1
12	9	1.7	539	4	US-09-389-681-311	Sequence 311, Appl1

13	539	4	US-09-620-405B-311	App1	Sequence 311, App1
14	539	4	US-09-339-33B-311	App1	Sequence 311, App1
15	539	4	US-09-433-826B-311	App1	Sequence 311, App1
16	539	4	US-09-604-287A-311	App1	Sequence 311, App1
17	539	4	US-09-634-759-311	App1	Sequence 311, App1
18	944	4	US-09-971-671B-110	App1	Sequence 11, App1
19	1238	2	US-08-510-290-111	App1	Sequence 11, App1
20	1238	4	US-09-702-705-803	App1	Sequence 803, App1
21	1238	4	US-09-736-457-803	App1	Sequence 803, App1
22	1238	4	US-09-614-124B-803	App1	Sequence 803, App1
23	1238	4	US-09-671-325-803	App1	Sequence 803, App1
24	1238	4	US-09-589-184-803	App1	Sequence 803, App1
25	1615	4	US-09-702-705-801	App1	Sequence 801, App1
26	1615	4	US-09-736-457-801	App1	Sequence 801, App1
27	1615	4	US-09-614-124B-801	App1	Sequence 801, App1
28	1615	4	US-09-671-325-801	App1	Sequence 801, App1
29	1615	4	US-09-589-184-801	App1	Sequence 801, App1
30	1987	2	US-08-990-379-1	App1	Sequence 1, App1
31	1993	2	US-09-016-434-1291	App1	Sequence 1291, App1
32	2000	4	US-09-702-705-825	App1	Sequence 825, App1
33	2064	4	US-09-736-457-825	App1	Sequence 825, App1
34	2064	4	US-09-614-124B-825	App1	Sequence 825, App1
35	2064	4	US-09-671-325-825	App1	Sequence 825, App1
36	2064	4	US-09-589-184-825	App1	Sequence 825, App1
37	2109	4	US-09-702-705-826	App1	Sequence 826, App1
38	2109	4	US-09-736-457-826	App1	Sequence 826, App1
39	2109	4	US-09-614-124B-826	App1	Sequence 826, App1
40	2109	4	US-09-671-325-826	App1	Sequence 826, App1
41	2109	4	US-09-589-184-826	App1	Sequence 826, App1
42	2240	4	US-09-016-434-1100	App1	Sequence 1100, App1
43	2240	4	US-09-702-705-804	App1	Sequence 804, App1
44	4637	4	US-09-736-457-804	App1	Sequence 804, App1
45	1.7				

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494

Patent No. 6664089 ✓
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 2117, NOVEL DUAL SPECIFICITY
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

ORGANISM: Homo sapiens
US-09-816-494-3
Alignment Scores:

```

Area. No.: 488.00 Length: 193
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Beet Local Similarity: 100.00% Mismatches: 0
Query Match: 94.35% Indels: 0
DB: 4 Gaps: 0

```

```

Db      592 CCGAGCTTATCCCGAGCTCATCTTCTCGCTCCGTAATGACACTTTTGTG 651
Qy      70 Lys11LeuProTrpLeuAspLysSerValAspPhe11eGluValAlaValAspAen 89
Db      652 AAAATTTCCGCTGAGCAAAATCAGTATTTCTATGAGAAAGCAAAAGCTCCAT 711
Qy      90 GlyValLeuValHisCysLeuAlaGly11SerArgSerAlaTrp11eAla109
Db      712 GGAATGTTCTAGTGAAGTTTACGTGGATTTCCCGCTCCGCAACATCCATCCG 771
Qy      110 Tyr11MetLeuArgMetAspMetSerLeuAspGluAla17YrArgPheVal17eGluLys 129
Db      772 TACATCATGAGAGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAGAAAA 831
Qy      130 ArgProThr11eSerProAspPheAspPheLeuGlyGluLeuLeuAspTyrG11LysLys 149
Db      832 AGACTCTATATCTCCAACTCATATTTCTGGGCCAATCTCGACTATGAGAAAGAA 891
Qy      150 11eLysAsn11nTh-G1ValAspG1YProLysSerLeuLysLeuLeuH:slauGlu 169
Db      892 ATTAAAGACCAAGCTGAGCATCAAGGCCAAAGCAAACTCAAGCTGCTGACCTGAG 951
Qy      170 LysProAsnGluProValProAlaValSerGluGlyGluLysSerGluTrpProLeu 189
Db      952 AAGCCAAATTAACCTGCTGCTGCTCAAGAGGAGGAGAAAGGAGAGAGAGAGAG 1011
Qy      190 SerProProCysAlaAspSerAla17nSerGluAla1eGlyGlu1nArgProValH:sp 209
Db      1012 AGTCCACCTGAGCGAGCTGCTGCTCACTCAAGAGCGAGCGAGCAAAAGCCCGCATCC 1071
Qy      210 AlAspValProSerValProSerValGluProSerLeuLeuGluAspSerProLeuVal 229
Db      1072 GCCAGCGTCCGAGCGTCCAGCGCTGACCGTCCCTTTAGAGAGAGAGCGCGTGTGA 1131
Qy      230 GluAlaLeuSerGlyLeuH:slauSerAlaAspArgLeuGluAspSerAspLysLeuLys 249
Db      1132 CAGCGCTCAAGCGCTGACCTGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1191
Qy      250 ArgSerPheSerLeuAspLysLysSerValSerTyrSerAlaSerMetAla1eSerLeu 269
Db      1192 CGTTCCTCTCTGTGATATCAAAATCAGTTTCTATTCAGCGAGAGAGAGAGAGATCTTA 1251
Qy      270 HisG1YPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerTrpTrpLeuAsp 289
Db      1252 CATTGCTTCTCTCATCAAGAGAGAGCTTGAATTAATAAACCCTTCACTACCTGAT 1311
Qy      290 GlyTrpAspLysLeuGluGluPheSerProValGluLeuSerGluGlu1nTrpProGlu 309
Db      1312 GGAACCAACAGCTATGCAAGTTCTCCCTCTTCAAGAGATATCGAGAGAGAGAGAGAG 1371
Qy      310 ThrSerProAspLysGluGluAlaSerTyrLeuLysLysLeuGluTrpAlaArgProSer 329
Db      1372 ACCAGTCTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
Qy      330 AspSerGluSerLysArgLeuH:slauSerValArgTrpSerSerSerGlyTrpAlaGluArg 349
Db      1432 GACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1491
Qy      350 SerLeuLeuSerProLeuH:slauSerGlySerValGluAspAspTyrH:slauSerPhe 369
Db      1492 TCCCTTTATCTCCAGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
Qy      370 LeuPheGlyLeuSerTrpSerGluGluH:slauTrpLysSerAlaGlyLeuGlyLysLys 389
Db      1552 CTTTCGAGCTTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1611
Qy      390 GlyTrpHisSerAspLysLeuAlaProGluTrpSerTrpProSerLeuTrpSerSerTrp 409
Db      1612 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1671
Qy      410 TyrPheAlaTrpGluSerSerH:slauPheTyrSerAlaSerAla1e1eTyrGlyLysAla 429

```

```

Db      1672 TACTTGCACAGAGCTCTCACTTACTCTGCTCAGCCATCTAGAGAGAGAGAGAG 1731
Qy      430 SerTyrSerAlaTyrSerCysSerGluLeuProTrpCysGlyAspGluValTyrSerVal 449
Db      1732 AGTTACTGCTGCTTACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1791
Qy      450 ArgArgArgGluLysProSerAspArgAlaAspSerArgTyrSerTrpHisGluGluSer 469
Db      1792 CGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1851
Qy      470 ProPheGluLysGluPheLysArgArgSerCysGluMetGluPheGlyGluSer11Met 489
Db      1852 CCGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1911
Qy      490 SerGluAspArgSerArgGluGluLysValGlySerGluSerSerPheSerGly 509
Db      1912 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1971
Qy      510 SerMetGluLeu11eGluValSer 517
Db      1972 AGCATGGAATCATGAGAGTCTCC 1995

RESULT 2
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 2117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,658
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589) ... (2563)
US-09-816-494-1

Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 94.35% Gaps: 0

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)
Qy      30 GluLeuMetGluGluAsnGly11eGlyTyrValLeuMetAlaSerAenTrpCysProLys 49
Db      1120 GAGCTATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1179
Qy      50 ProAspPhe11eProGluSerH:slauPheLeuArgValProValAspAspPheCysGlu 69
Db      1180 CCGACTTATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1239
Qy      70 Lys11LeuProTrpLeuAspLysSerValAspPhe11eGluValAlaValAspAen 89
Db      1240 AAAATTTCCGCTGAGCAAAATCAGTATTTCTATGAGAAAGCAAAAGCTCCAT 1299
Qy      90 GlyValLeuValHisCysLeuAlaGly11SerArgSerAlaTrp11eAla109
Db      1300 GGAATGTTCTAGTGAAGTTTACGTGGATTTCCCGCTCCGCAACATCCATCCG 1359
Qy      110 Tyr11MetLeuArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129

```

```

Db      592 CCGACCTTATCCCGACCTCATCTTCTCGCTGCTGTAAGTACAGCTTTTGAG 651
Qy      70  Lys1LeuProTTPLeuAplySerValAspPhe1Leg1uValAlaValAspAra 89
Db      652 AAAATTTGCGCTGCTGACAAATCAGTATGATTTCTAGGAAGCAAAAGCTTCAT 711
Qy      90  GlyValAlaValAlaHisCysLeuAlaGly1LeuSerArgSerAlaThr1Lea1Ala1a 109
Db      712 GGAATGTTCTAGTGAGCTTTAGCTTGGATCTCCCGCTCCGACCAATGCTATCGCC 771
Qy      110 Tyr1LeuMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheVal1uValuys 129
Db      772 TACATCATAGAGAGATGACATGCTTTTATGATGAGCTTACAGATTTGTAAGAGAAA 831
Qy      130 ArgProThr1LeuSerProAsnPhaAsnPhaLeuGlyGlnLeuLeuAspTyrG1uValuys 149
Db      832 AGACCTACTATATCTCCAAACTCAATTTCTGGGCCAACTCTCGACTATGAGAAAGAG 891
Qy      150 1LeuValAsnGlnThsGlyAlaSerGlyProLysSerLysLeuLysLeuLys1u 169
Db      892 ATTAGAACCAAGCTGAGCATCAAGGCGCAAAAGCAATCAAGCTGACCTGAG 951
Qy      170 LysProAsnGluProValProAlaValSerGlyGlyGlnLysSerGluThsProLys 189
Db      952 AAGCAAAATGACCTGCTCTCTCTCTCAAGAGG1GAGCAAAAGCGAGAGCCCTC 1011
Qy      190 SerProProCysAlaAspSerAlaThsSerGluAlaGlyGlnArgProVal1uAsp 209
Db      1012 AGTCACCTCTGCTCCCACTGCTACTCACTGAGAGCGAGCAAAAGCCCGGACTCC 1071
Qy      210 AlaSerValProSerValProSerValGlnProSerLeuGluAspSerProLeuVal 229
Db      1072 GCCGCGCTGCCAGCGCTGCGAGGCTGACCGCTCTGTTAGAGGACAGCGCTGCTGA 1131
Qy      230 G1uAlaLeuSerGlyLysLeuLysSerValAspArgLysGluAspSerAsnLysLeuys 249
Db      1132 CAGCGCTCAAGTGGGCTGACCTGCTCCGCAAGAGCTGAGAGCAACATTAAGCTCAAG 1191
Qy      250 ArgSerPheSerLeuAsp1LeuLysSerValSerTyrSerAlaSerMetAla1AspLeu 269
Db      1192 CGTTCCTCTCTCTGATATCAATCAAGTTTATATTCAGCGAGAGAGGAGCACTCTTA 1251
Qy      270 HisGlyPheSerSerSerGlyLysAspAlaLeuGlyTyrTyrLysProSerThsLeuAsp 289
Db      1252 CATGCTCTCTCTCATCAAGAGATGCTTGAAATACTAACAACTTCCACTACTGAT 1311
Qy      290 G1uThsAsnLysLeuGlyGlnPheSerProValGlnLysSerGluGlnThsProGlu 309
Db      1312 GGGACCAAGCAAGCTATGCAAGTCTCTCCCTGTTCAAGACTATCGAGAGAGACTCCGAA 1371
Qy      310 ThsSerProAspLysGluGluAlaSerTyrLeuLysLeuGlnThsAlaArgProSer 329
Db      1372 ACCAGCTCTGATAGAGAGAGAGCAAGATCCCAAGAGAGCTGAGAGCGGAGCGCTTA 1431
Qy      330 AspSerGlnSerLysArgLysLeuLysSerValArgThsSerSerSerGlyThsAlaGlnArg 349
Db      1432 GACAGCGCAAGCAAGGATGCTATCGGTGAGAAACCAAGAGAGAGTGGACCGCCGAGAG 1491
Qy      350 SerLeuLysSerProLeuHisArgSerGlySerValGluAspArgTyrHs1SerPhe 369
Db      1492 TCCCTTTATCTCCACTGATCGAAGTGGAGGCTGAGAGCAATTAACCAACCACTTC 1551
Qy      370 LeuPheGlyLysSerThsSerGlnGlnHisLeuThsLysSerAlaGlyLysGlyLys 389
Db      1552 CTTTCGCGCTTTCCCAAGCAAGCAAGCACTTCAAGATCTGCTGCGCTGGGCTTAAG 1611
Qy      390 GlyTyrHisSerAsp1LeuAlaProGlnThsSerThsProSerLeuThsSerSerTTP 409
Db      1612 GCGCGGACCTCGAATCTTACCTGCCCCCAAGCTTACCCCTCCGAGACCAAGACTG 1671
Qy      410 TyrPheAlaThsGlySerSerHisPheTyrSerAlaSerAla1LeuTyrGlyLysAla 429

```

```

Db      1672 TATTTTGCAAGAGTCTCACTTCTACTGCTGACCACTTACGAGGAGCTGCC 1731
Qy      430 SerTyrSerAla1TyrSerCysSerGlnLeuProThsCysGlyAspGlnVal1TyrSerVal 449
Db      1732 AGTTACTCTGCTACAGCTGAGCGAGCGAGCTGCCACTCTCGAGAGCAAGCTTATCTTG 1791
Qy      450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgValArgSerTyrHisGluGlnSer 469
Db      1792 CGCAGCGCGCAAGACCAAGTGAAGAGAGCTGACTCGCGCGCACTGCAATGAGAGAGACC 1851
Qy      470 ProPheGlyLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSer1LeuMet 489
Db      1852 CCGTTGAAAAGCACTTTAAACCGCAAGCTGCAATGAAATTTGAGAGAGCACTATG 1911
Qy      490 SerGluAsnArgSerArgGluGluLysLeuValGlySerGlnSerSerPheSerGly 509
Db      1912 TCAGAGAACAGGTCAAGGAGAGCTGGGAGAAAGTGGGAGAGTCACTTATCTTGGGAC 1971
Qy      510 SerMetGlu1Leu1Leg1uValSer 517
Db      1972 ACCATGAAATCATTAAGCTCTCC 1995

RESULT 2
US-09-816-494-1
Sequence 1 Application US/09816494
Patent No. 664088
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38652 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR APPLICATION NUMBER: 2001-03-23
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589) ... (2563)
US-09-816-494-1

Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
Gaps: 0

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)
Qy      30  GluLeuMetGlnGlnAlaAsnGly1Leg1uValLeuAlaSerAsnThsCysProLys 49
Db      1120 GAGCTATGACCAAGAAATGAGATGGTATGTTGTTAAATGCCAACAATACCTTCCAAAG 1179
Qy      50  ProAspPhe1LeuProGluSerHisPheLeuArgVal1ProValAsnAspSerPheCysGlu 59
Db      1180 CCGACTTATCCCGGATCTCATCTTCTCGCGTGGCGCGGAGTGAATGACAGCTTTTGAG 1239
Qy      70  Lys1LeuProTTPLeuAplySerValAspPhe1Leg1uValAlaValAspAra 89
Db      1240 AAAATTTGCGCTGCTGACAAATCAGTATGATTTCTAGGAAGCAAAAGCTTCAT 1299
Qy      90  GlyValAlaValAlaHisCysLeuAlaGly1LeuSerArgSerAlaThr1Lea1Ala1a 109
Db      1300 GGAATGTTCTAGTGAGCTTTAGCTTGGATCTCCCGCTCCGACCAATGCTATCGCC 1359
Qy      110 Tyr1LeuMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheVal1uValuys 129

```

DB 1360 TACATATATAGAGATGACATCTCTTATGATGAGCTTCACATTTTGGAGAGAAAA 1449
QY 130 ATGProThr1LeSerProAsnPhenAlaLeuGlyGlnLeuLeuAlaPyrGlnLeuLeu 149
DB 1420 AGACCTACTATATCTCCAACTTCAATTTCTGGGCGCAACTCTGAGCTATGAGAAAG 1479
QY 150 TLeAsnGlnThrGlyAlaSerGlyProLysSerLeuLeuLeuLeuLeuLeu 169
DB 1480 ATTAAGAACCAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1539
QY 170 LysProAsnGlnProValProAlaValSerGlnGlyGlnLeuLeuLeuLeuLeu 189
DB 1540 AACCCAAATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1599
QY 190 SerProProCysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnAlaProValHisPro 209
DB 1600 AGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGlnLysProLeuVal 229
DB 1660 GCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTG 1719
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspAlaGlyLeuGlnLysSerAlaLeu 249
DB 1720 CAGGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1779
QY 250 ArgSerPheSerLeuAspIleLysSerValSerValSerValSerValSerValSer 269
DB 1780 CGTCTCTCTCTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1839
QY 270 HisGlyPheSerSerSerSerGlnAlaGlnGlyGlyGlyGlyGlyGlyGlyGlyGly 289
DB 1840 CATGCT 1899
QY 290 GlyThrAlaLeuLeuGlyGlnPheSerProValGlnGlnLeuSerGlnGlnThrProGln 309
DB 1900 GGGACCAACAAAGCTATCCAGCTCTCCCTGCTGCAAGCAATCCAGCAAGCTCCCA 1959
QY 310 ThrSerProAspLysGlnGlnAlaSerIleProLysLeuGlnThrAlaAspProSer 329
DB 1960 ACCAGCTCTGATTAAG 2019
QY 330 AspSerGlnSerLysAlaGlyLeuHisSerValAlaGlyThrSerSerSerGlyThrAlaGln 349
DB 2020 GACAGCAG 2079
QY 350 SerLeuLeuSerProLeuHisAlaGlySerValGlnLysAlaPheThrHisSerPhe 369
DB 2080 TCCCTTTATCTTCACTGATCCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2139
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
DB 2140 CTTTTCGAGCTTTCACACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2199
QY 390 GlyTPHAspSerAlaIleAlaProGlnThrSerThrProSerLeuThrSerSerThr 409
DB 2200 GGTGCGACCTCGATATCTTGGCCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2259
QY 410 TyrPheAlaThrGlnLysSerThrHisPheThrSerAlaSerAlaIleThrGlyGlySerAla 429
DB 2260 TATTTGCGACAGAGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2319
QY 430 SerTyrSerAlaLysSerCysSerGlnLeuProThrCysGlnLysAlaValTyrSerVal 449
DB 2320 ACTTACTCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2379
QY 450 ATG 459
DB 2380 CCGAGGCGGAG 2439
QY 470 ProPheGlnLysGlnLysThrLysArgArgSerCysGlnThrGlnLysGlnLysThr 469

DB 2440 CCCTTGAAG 2499
QY 490 SerGlnAsnArgSerArgGlnGlnLeuGlyLysValGlnLysSerGlnSerPheSerGly 509
DB 2500 TCGAG 2559
QY 510 SerMerGlnLysIleGlnValSer 517
DB 2560 AGCATGAG 2583
RESULT 3
US-09-920-668-3
Sequence 3, Application US/09920668
Patent No. 6482644
GENERAL INFORMATION:
APPLICANT: Brett P. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
FILE REFERENCE: RFS-0246
CURRENT APPLICATION NUMBER: US/09/920,668
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENGTH: 2377
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (135)...(2012)
US-09-920-668-3
Alignment Scores:
Pred. No.: 2,786-10 Length: 2377
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.87% Indels: 0
DB: 4 Gaps: 0
US-09-964-277-21 (1-517) x US-09-920-668-3 (1-2377)
QY 94 VAIHAGVLeuAlaGlyLysSerArgSerAlaThrIleAlaIleAlaThrIleMetLys 113
DB 864 GTCCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923
RESULT 4
US-09-016-434-1135
Sequence 1135, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 FORSTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: